IN THE SPECIFICATION

Please amend the specification as shown:

Please delete the paragraph on page 9, line 5 to page 10, line 5 and replace it with the following paragraph:

The vector can be any useful vector known to the ordinary artisan, including, but not limited to, a cloning vector, an insertion vector, or an expression vector. Examples of vectors include plasmids, phages, cosmids, phagemid, yeast artificial chromosome (YAC), bacterial artificial chromosome (BAC), human artificial chromosome (HAC), viral vector, such as adenoviral vector, retroviral vector, and other DNA sequences which are able to replicate or to be replicated *in vitro* or in a host cell, or to convey a desired DNA segment to a desired location within a host cell.

According to a preferred embodiment of the invention, the recombinant vector is a BAC pBeloBAC11 in which the genomic region of *Mycobacterium bovis-BCG* 1173P3 that spans the region corresponding to the locus 1,760,753 bp to 1,830,364 bp in the genome of *M. tuberculosis* H37Rv has been inserted into the HindIII restriction site; this recombinant vector is named X229. In this region, the inventors have demonstrated the deletion of a 2153 bp fragment, corresponding to SEQ ID N°4, in the vast majority of *M. tuberculosis* strains excepted strains of *M. tuberculosis* having the sequence CTG at codon 463 of gene *katG* and having no or very few IS6110 sequences inserted in their genome. That's the reason why the inventors named this deletion of 2153 bp TbD1 ("*M. tuberculosis* specific deletion 1"). TbD1 is flanked by the sequence GGC CTG GTC AAA CGC GGC TGG ATG CTG **(SEQ ID NO: 23)** and AGA TCC GTC TTT GAC ACG ATC GAC G **(SEQ ID NO: 24)**. External primers hybridizing with such sequences outside

TbD1 or the complementary sequences thereof can be used for the amplification of TbD1 to check for the presence or the absence of the deletion of the TbD1. The inventors design for example the following primers:

5'- CTA CCT CAT CTT CCG GTC CA-3' (SEQ ID N°17)

5'- CAT AGA TCC CGG ACA TGG TG-3'(SEQ ID N°18)

In order to get a specific 500 pb probe for hybridization experiments, a PCR amplification of a fragment comprised in TbD1 may be realized by using the plasmid X229 as a matrix. The amplification of a fragment of approximatively 500 bp contained in TbD1 can be performed by using the following primers:

5'- CGT TCA ACC CCA AAC AGG TA-3' (SEQ ID N°13)

5'- AAT CGA ACT CGT GGA ACA CC-3' (SEQ ID N°14)

The amplification of a fragment of approximatively 2,000 bp contained in TbD1 can be performed by using the following primers:

5'- ATT CAG CGT CTA TCG GTT GC-3' (SEQ ID N°15)

5'- AGC AGC TCG GGA TAT CGT AG-3' (SEQ ID N°16)

The PCR conditions are the following: denaturation 95°C 1 min, then 35 cycles of amplification [95°C during 30 seconds, 58°C during 1 min] , then elongation 72°C during 4 min.

Please delete the paragraph on page 20, lines 26-31 and replace it with the following paragraph:

Figure 2 : Sequences **(SEQ ID NOS 116-117)** in the TbD1 region obtained from strains of various geographic regions.

* refers to groups based on *katG*^{c463}/*gyrA*^{c95} sequence polymorphism defined by Sreevatsan and colleagues (Ref. 2). Numbers correspond to strain designation used in

Kremer et al. (1999, J. Clin Microbiol. 37: 2607-2618) (Ref. 8) and Supply et al (2001, J. Clin. Microbiol. 39: 3563-3571) (ref.9).

Please delete the paragraph on page 21, line 33 to page 22, line 4 and replace it with the following paragraph:

Figure 6 : Sequence **(SEQ ID NO: 19)** of the specific insertion element in genome of *Mycobacterium canettii* strains. The beginning of this insertion element is at position 399 and the end of this insertion element is at position 2378. This insertion element contains the coding sequence of a putative transposase (sequence in bold characters, from position 517 to position 2307) that shows significant homology with a transposase of *Mycobacterium smegmatis*. This coding sequence is framed by two 20 bp inverted repeats (sequences underlined from position 399 to 418 and from position 2359 to 2378).

Please delete Table 1 on pages 36-39 and replace it with the following Table:

Table 1: RD, RvD and TbD1 regions and selected primers

Region absent from BCG	**Gene**	**Size (kb)**	**Internal Primerpair**	**Flanking primers or 2nd internal * primerpair**

RD1	Rv3871-Rv3879c	9.5	RD1in-Rv3878F GTC AGC CAA GTC AGG CTA CC **(SEQ ID NO: 25)**	RD1-flank.left GAA ACA GTC CCC AGC AGG T **(SEQ ID NO: 26)**
			RD1in-Rv3878R CAA CGT TGT GGT TGT TGA GG **(SEQ ID NO: 27)**	RD1-flank.right TTC AAC GGG TTA CTG CGA AT **(SEQ ID NO: 28)**
RD2	Rv1978-Rv1988	10.8	RD2-Rv1979.int.F TAT AGC TCT CGG CAG GTT CC **(SEQ ID NO: 29)**	RD2-flank.F CTC GAC CGC GAC GAT GTG C **(SEQ ID NO: 30)**
			RD2-Rv1979-int.R ATC GGC ATC TAT GTC GGT GT **(SEQ ID NO: 31)**	RD2-flank.R CCT CGT TGT CAC CGC GTA TG **(SEQ ID NO: 32)**
RD3*	Rv1573-Rv1586c	9.2	RD3-Rv1586.int.F TTA TCT TGG CGT TGA CGA TG **(SEQ ID NO: 33)**	RD3-int-REP.F CTG ACG TCG TTG TCG AGG TA* **(SEQ ID NO: 34)**

			RD3-Rv1586.int.R CAT ATA AGG GTG CCC GCT AC **(SEQ ID NO: 35)**	RD3-int-REP.R GTA CCC CCA GGC GAT CTT* **(SEQ ID NO: 36)**
RD4	Rv1505c-Rv1516c	12.7	RD4-Rv1516.int.F CAA GGG GTA TGA GGT TCA CG **(SEQ ID NO: 37)**	RD4-flank.F CTC GTC GAA GGC CAC TAA AG **(SEQ ID NO: 38)**
			RD4-Rv1516.int.R CGG TGA TTC GTG ATT GAA CA **(SEQ ID NO: 39)**	RD4-flank.R AAG GCG AAC AGA TTC AGC AT **(SEQ ID NO: 40)**

Table 1 (continued)

RD5*	Rv2346c-Rv2353c	9.0	RD5A-Rv2348.int.F AAT CAC GCT GCT GCT ACT CC **(SEQ ID NO: 41)**	RD5B-plcA.int.F CAA GTT GGG TCT GGT CGA AT **(SEQ ID NO: 42)**
			RD5A-Rv2348.int.R GTG CTT TTG CCT CTT GGT C **(SEQ ID NO: 43)**	RD5B-plcA.int.R GCT ACC CAA GGT CTC CTG GT **(SEQ ID NO: 44)**

RD6*	Rv3425-Rv3428c	4.9	RD6-IS1532F CAG CTG GTG AGT TCA AAT GC **(SEQ ID NO: 45)**	ND
			RD6-IS1532R CTC CCG ACA CCT GTT CGT **(SEQ ID NO: 46)**	ND
RD7	Rv1964-Rv1977	12.7	RD7-Rv1976.int.F TGG ATT GTC GAC GGT ATG AA **(SEQ ID NO: 47)**	RD7-flank.F GGT AAT CGT GGC CGA CAA G **(SEQ ID NO: 48)**
			RD7-Rv1976.int.R GGT CGA TAA GGT CAC GGA AC **(SEQ ID NO: 49)**	RD7-flank.R CAG CTC TTC CCC TCT CGA C **(SEQ ID NO: 50)**
RD8	*ephA-lpqG*	5.9	RD8-ephA.F GGT GTG ATT TGG TGA GAC GAT G **(SEQ ID NO: 51)**	RD8-flank.F CAA TCA GGG CTG TGC TAA CC **(SEQ ID NO: 52)**

			RD8-ephA.R	RD8-flank.R
			AGT TCC TCC TGA	CGA CAG TTG TGC
			CTA ATC CAG GC	GTA CTG GT **(SEQ**
			(SEQ ID NO: 53)	**ID NO: 54)**
RD9	*cobL*-Rv2075	2.0	RD9-intF	RD9-flankF
			CGA TGG TCA ACA	GTG TAG GTC AGC
			CCA CTA CG	CCC ATC C
			(SEQ ID NO: 55)	**(SEQ ID NO: 56)**
			RD9-intR	RD9-flankR
			CTG GAC CTC GAT	GCC CAA CAG CTC
			GAC CAC TC	GAC ATC
			(SEQ ID NO: 57)	**(SEQ ID NO: 58)**
RD10	Rv0221-Rv0223	1.9	RD10-intF	RD10-flankF
			GTA ACC GCT TCA	CTG CAA CCA TCC
			CCG GAA T	GGT ACA C
			(SEQ ID NO: 59)	**(SEQ ID NO: 60)**
			RD10-intR	RD10-flankR
			GTC AAC TCC ACG	GTC ATG AAC GCC
			GAA AGA CC	GGA CAG
			(SEQ ID NO: 61)	**(SEQ ID NO: 62)**

RD11	Rv2645-Rv2695c	11.0	RD11-Rv2646F CGG CAG CTA GAC GAC CTC **(SEQ ID NO: 63)**	RD11-fla-F TCA CAT AGG GGC TGC GAT AG **(SEQ ID NO: 64)**
			RD11-Rv2646R AAC GTG CTG CGA TAG GTT TT **(SEQ ID NO: 65)**	RD11-fla-R AGA GGA ACC TTT CGG TGG TT **(SEQ ID NO: 66)**
RD12	*sseC*-Rv3121	2.8	RD12-Rv3120.int.F GAA ATA CGA GTG CGC TGA CC **(SEQ ID NO: 67)**	RD12-flank.F GCC ATC AAC GTC AAG AAC CT **(SEQ ID NO: 68)**
			RD12-Rv3120.int.R CTC TGA ACC ATC GGT GTC G **(SEQ ID NO: 69)**	RD12-flank.R CGG CCA GGT AAC AAG GAG T **(SEQ ID NO: 70)**
RD13	Rv1255c-Rv1257c	3.0	RD13intF GGA TGT CAC TCG GAA CGG CA **(SEQ ID NO: 71)**	RD13-flank.F CGA TGG TGT TTC TTG GTG AG **(SEQ ID NO: 72)**

			RD13intR	RD13-flank.R
			CAC CGG GCT GAT CGA GCG A **(SEQ ID NO: 73)**	GGA TCG GCT CAG TGA ATA CC **(SEQ ID NO: 74)**
RD14	Rv1765c-Rv1773c	9.0	RD14-Rv1769.int.F GTG GAG CAC CTT GAC CTG AT **(SEQ ID NO: 75)**	RD14-flankF TTG ATT CGC CAA CAA CTG AA **(SEQ ID NO: 76)**
			RD14-Rv1769.int.R CGT CGA ATA CGA GTC GAA CA **(SEQ ID NO: 77)**	RD14-flankR GGG CTG GTT AGT GTC GAT TC **(SEQ ID NO: 78)**

Table 1 (continued)

Region missing from *M. tuberculosis* H37Rv

RvD1*		5.0	RvD1-int1F AGC GCG TCG AAC ACC GGC **(SEQ ID NO: 79)**	RvD1-int2.F GAG CCA CTC CGA TGT TGA CT **(SEQ ID NO: 80)**
			RvD1-int1R CCT GAA TCC GCG CAA TTC CAT **(SEQ ID NO: 81)**	RvD1-int2.R CAC GCG AAC CCT ACC TAC AT **(SEQ ID NO: 82)**

RvD2*	*plcD*	5.1	RvD2-int1F GTT CTC CTG TCG AAC CTC CA **(SEQ ID NO: 83)**	RvD2-int2F GGA CGG TGA CGG TAT TTG TC **(SEQ ID NO: 84)**
			RvD2-int1R ACT TCA CCG GTT TCA TCT CG **(SEQ ID NO: 85)**	RvD2-int2R TCG CCA ACT TCT ATG GAC CT **(SEQ ID NO: 86)**
RvD3		1.0	RvD3-intF ATC GAT CAG GTC GTC AAT GC **(SEQ ID NO: 87)**	RvD3-flank.F AAA CCA TGC AGC GTC TGC CA **(SEQ ID NO: 88)**
			RvD3-intR ACG CCA CCA TCA AGA TCC **(SEQ ID NO: 89)**	RvD3-flankR GCG TTT CTG CGT CTG GTT GA **(SEQ ID NO: 90)**
RvD4*	PPE gene	0.8	RvD4-intF-PPE GGT TGC CAA CGT TAC CGA TGC **(SEQ ID NO: 91)**	ND

			RvD4-intR-PPE	ND
			CCG GTG GTG GTG	
			GCG GCT	
			(SEQ ID NO: 92)	
RvD5	*moa*	4.0	RvD5intF	RvD5-flankF
			GGG TTC ACG TTC	CCC ATC GTG GTC
			ATT ACT GTT C	GTT CAC C
			(SEQ ID NO: 93)	**(SEQ ID NO: 94)**
			RvD5intR	RvD5-flankR
			CCT GCG CTT ATC	GTA CCC GCA CCA
			TCT AGC GG	CCT GCT G
			(SEQ ID NO: 95)	**(SEQ ID NO: 96)**
TbD1	*mmpL6*	2.1	TBD1intS.F	TBD1fla1-F
			CGT TCA ACC CCA	CTA CCT CAT CTT
			AAC AGG TA	CCG GTC CA **(SEQ**
			(SEQ ID NO: 97)	**ID NO: 98)**
			TBD1intS.R	TBD1fla1-R
			AAT CGA ACT CGT	CAT AGA TCC CGG
			GGA ACA CC	ACA TGG TG **(SEQ**
			(SEQ ID NO: 99)	**ID NO: 100)**

***katG, gyrA, oxyR', pncA* and *mmpL6* PCR and sequencing primers**

katG^{463}	*katG*-2154,225-PCR-F CTA CCA GCA CCG TCA TCT CA **(SEQ ID NO: 101)**	*katG*-2154,872-SEQ- R ACA AGC TGA TCC ACC GAG AC **(SEQ ID NO: 102)**
	katG-2155,157-PCR-R AGG TCG TAT GGA CGAACA CC **(SEQ ID NO: 103)**	
gyrA^{95}	*gyrA*-7,127-PCR-F GTT CGT GTG TTG CGT CAA GT **(SEQ ID NO: 104)**	*gyrA*-7,461F CGG GTG CTC TAT GCA ATG TT **(SEQ ID NO: 105)**
	gyrA- 8,312-PCR-R CAG CTG GGT GTG CTT GTA AA **(SEQ ID NO: 106)**	
oxyR^{285}	*oxyR* 2725,559F TAT GCG ATC AGG CGT ACT TG **(SEQ ID NO: 107)**	*oxyR*-2726,024-SEQ- R CAA AGC AGT GGT TCA GCA GT **(SEQ ID NO: 108)**

		oxyR-2726,024-PCR-R CAA AGC AGT GGT TCA GCA GT **(SEQ ID NO: 109)**	

Table 1 (continued)

pncA[57]		*pncA*–2288,678-PCR-F ATC AGG AGC TGC AAA CCA AC **(SEQ ID NO: 110)**	*pncA*- 2289,319-SEQ-R GGC GTC ATG GAC CCT ATA TC **(SEQ ID NO: 111)**
		pncA- 2289,319-PCR-R GGC GTC ATG GAC CCT ATA TC **(SEQ ID NO: 112)**	
mmpL6[551]		*mmpL*-seq5F GTA TCA GAG GGA CCG AGC AG **(SEQ ID NO: 113)**	*mmpL*-seq5F GTA TCA GAG GGA CCG AGC AG **(SEQ ID NO: 114)**
		TBD1fla1-R CAT AGA TCC CGG ACA TGG TG **(SEQ ID NO: 115)**	

The RD nomenclature used in this table is based on that used by Brosch *et al.* (2000), (Ref. 25) and differs from that proposed by Behr and coworkers (1999), (Ref. 6). Primer sequences are shown in 5' →3' direction.

* Regions where a second pair of internal primers was used rather than flanking primers, due to flanking repetitive regions, and/or mobile genetic elements.